My Family Pedigree

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Genetics is an ever-expanding field of research. The genetic field has rapidly expanded from Mendel's studies to genetically modified treatments, multi-allele variation knowledge, and studies on epigenetic influences. This research is a Participant Observational study conducted with my immediate biological family in a four-generational pedigree. My pedigree includes 38 subjects. I collected the following: 1) attached or unattached earlobes, 2) a longer second toe, 3) the ability to roll their tongue like a hot dog, 4) the ability to fold their tongue, 5) cleft chin, 6) mid-digit finger hair, and 7) dimples. I hypothesized that Mendelian inheritance would be followed in my pedigree. We found this to be true utilizing a two-sample t-test assuming equal variance within our total population for tongue rolling (P=0.002), tongue folding (P=0.015), mid-digit hair (P=0.095), and dimples (P=0.000). Earlobes, longer second toes, and a cleft chin did not meet statistical significance within the total population. Immediate family unit phenotypes were further tested based on their parents' genetic patterns (heterozygous vs homozygous predictions). This resulted in more consistent Mendelian inheritance. However, the dominant allele for dimples and longer second toes from both homozygous recessive parents did not follow this pattern. These non-Mendelian phenotypes are likely influenced by epigenetics, potential multi-allele variations, and/or birth defects. This study found limited Mendelian inheritance in the total subject population; however, it is more consistent with Mendelian inheritance when evaluating each immediate family unit within their pedigree.

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